First report of gastroenteritis by genotype G12 rotavirus in Dakar, Senegal

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Abstract

The genotype G12 rotavirus was isolated from the stool of children 5 years old or younger with acute gastroenteritis during 1 year in three Dakar hospitals. The G12 genotype was the most common (58.25%). VP4 genotyping revealed mixed genotypes (1.94%).

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Introduction

Human group A rotaviruses are ubiquitous and are the most frequent cause of diarrhoea in children worldwide. Their genome comprises 11 double-stranded RNA fragments [1]. The three main antigenic proteins of the virus can be used to classify rotavirus into seven groups labeled A to G (VP6), and into G (VP7) and P (VP4) genotypes [2]. This study reports on the isolation of rotavirus belonging to the G12 genotype from stool samples obtained from pediatric patients in Dakar.

Materials and methods

The study was performed during 13 consecutive months from February 2011 to February 2012. We examined the stool of all children between 0 and 5 years of age with acute gastroenteritis (AGE) that led to admission at one of the three hospitals engaged in the study: the Albert-Royer Children's Hospital, the Pediatric Institute of Pikine and the Abass Ndao Hospital.

One hundred three children were included. The stool samples were collected in sterile containers and immediately sent to the laboratory. An ELISA test (IDEIA Rotavirus; Dako, Glostrup, Denmark) was performed by the hospital laboratory to detect samples positive for group A rotavirus. Aliquots were prepared and sent to the laboratory of the Noguchi Memorial Institute for Medical Research, a regional reference center in Ghana, for detection of rotavirus by reverse transcriptase (RT) PCR. The strains were then analyzed by polyacrylamide gel electrophoresis (PAGE), followed by genotyping.

PAGE was performed on two polyacrylamide gels of different concentrations (10% and 3%). Extracted RNA was mixed with bromophenol blue and glycerol before loading onto the migration gel. The migration was performed in Tris–glycine buffer for 22 hours at 100 V. Bands were detected by silver staining, and the gel was subsequently placed between two cellophane sheets and put into a gel dryer for 90 minutes.

ELISA-positive samples for rotavirus were also tested for *VP7* and *VP4* genes by RT-PCR to classify strains. Virus RNA was extracted with the use of TRI-Reagent1 (Sigma, St Louis, MO, USA) according to the method of Chomczynski and Sacchi [3]. A mixture was added to the denatured RNA for RT. A first PCR was carried out with all of the RT product. The PCR product was subjected to a second amplification by heminested multiplex PCR with internal primers which could amplify VP7 genotypes G1, G2, G3, G4, G8, G9, G10, G12 and VP4 genotypes P[4], P[6], P[8], P[9], P[10], P[11] [4,5].

Statistical analysis was carried by Epi Info 7 software (US Centers for Disease Control and Prevention, Atlanta, GA, USA).

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Results

One hundred three stool samples positive for rotavirus were detected by ELISA. These were derived from children less than 1 month old to 5 years of age, with a sex ratio (M/F) of 1.39. Their AGE occurred during the months of December, January and February. Of these samples, 65 (63.10%) were positive by PAGE, of which 50 were short electropherotypes and 15 were long electropherotypes.

The VP7 genotyping yielded two genotypes: G12 and G1 with a predominance of the G12 genotype (60/103, 58.25%). Forty-two strains could not be genotyped by VP7 (40.77%). The VP4 genotyping revealed two different genotypes: P[8] (73.78%) and P[6] (24.27%), as well as mixed genotypes P[8] + P[6] (1.94%).

Simultaneous VP7 and VP4 genotyping allowed several types of associations to be uncovered: the predominant G12P[8] association (49.51%), followed by G12P[6] association (7.76%) (Table 1).

Discussion

Rotaviruses represent the primary cause of AGE in the world [2]. They cause 42% of all AGE that requires hospitalization, and they are involved in 23% of community-based AGE in developed countries [2]. In Senegal, there have been few studies of rotavirus-induced diarrhoea, and to our knowledge, our study is the first to report the isolation of G12 genotype rotavirus from pediatric patients. This genotype, which was predominant in our study, has already been isolated in the West African subregion, in Niger [5] and Nigeria [6] in particular. It has similarly been reported in studies undertaken in Cameroon [7], Vietnam [8] and Hungary [9].

This genotype tends to dominate other genotypes on a more or less worldwide scale, which could have implications for vaccination strategies [9].

TABLE 1. Genotype distribution of rotavirus strains in children 5 years old and younger

	P genotypes			
G genotypes	**P[6]**	**P[8]**	**P[6] + P[8]**	**Total**
G1		1		1
G12	8	51	1	60
NGT	17	24	1	42
Total	25	76	2	103

NGT, not genotyped (untypable strain).

The co-circulation of numerous electrophoretic profiles as observed in our study has also been described by other investigators [1]. This is characteristic of the epidemiology of rotavirus infections.

We have encountered mixed profiles, as reported previously in several studies [8]. These mixed profiles are frequent during epidemics and are indicative of mixed infections in the same child, which may be the result of a genetic rearrangement mechanism [1].

The VP4 genotyping mainly yielded P[8] genotypes, which is comparable to the results obtained by other investigators [8,9]. Similarly, the predominance of the G12P[8] association noted in our study has also been reported by other investigators [8,9].

In conclusion, this study has shown that G12 genotype rotavirus circulates in Senegal in parallel with mixed genotypes. The latter promotes the emergence of new strains, and therefore regular monitoring of circulating strains in the country is reasonable. Multicentre studies undertaken throughout the country will allow for a better appreciation of the extent of circulation of the viruses responsible for AGE in general and the G12 genotype rotavirus in particular.

Conflict of Interest

None declared.

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